

**REMARKS**

The specification has been amended to recite the SEQ ID Numbers for the nucleic acid sequence of Genbank Accession No. X69322 and the amino acid sequence encoded thereby.

Claims 1, 2, 7 and 18 have also been amended to obviate the 35 U.S.C. §112, second paragraph rejection set forth in the present Official Action.

All of the foregoing amendments are presented to further clarify the scope of the invention and in no way represent acquiescence to the rejections made by the Examiner.

The April 11, 2003 Official Action and references cited therein have been carefully reviewed. In light of the amendments presented herewith and the following remarks, favorable reconsideration and allowance of the application are respectfully requested.

At the outset, the Examiner indicates at page 7 that claims 12, 16-18, 20-22, 29, and 30 are deemed free of the prior art. Notably, claim 2 has been rejected under 35 U.S.C. §112, second paragraph only. Accordingly, Applicants assume that claim 2 is also free of the prior art.

At page 3 of the Official Action, the Examiner maintains the rejection of claims 17 and 30 under 35 U.S.C. §112, first paragraph as allegedly containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention. Applicants again reiterate that the INRA clone of claims 17 and 30 is readily available to the public and further that this particular clone is not essential to the practice of the instant invention. Attached hereinwith, please find two references where clone INRA 717 1-B4 was used, Siebrecht et al. *Journal of experimental Botany* 1999;50(341):1797-1806 and Lapierre et al. *Plant Physiology* 1999;119:153-163. However,

in order to advance prosecution, these claims are cancelled in accordance with the present amendment.

At page 3, the Examiner indicates that claims 2, 7-12, 16-18, 20-22, and 29-30 remain rejected under 35 U.S.C. §112, second paragraph, for the reasons set forth in the Official Action of July 8, 2002. However, it is noted that the Examiner has stated that the previous rejection of claims 7, 12-27, 31, and 40 under 35 U.S.C. §112, second paragraph, has been withdrawn in view of Applicant's amendments. While the current Official Action provides a basis for the rejection of claims 2, 7, 11, 12, 18, 19, and 21 under 35 U.S.C. §112, second paragraph, the Action is silent regarding the grounds for the assertion that claims 8, 9, 10, 16, 17, 20, 22, 29, and 30 are lacking in clarity. Clarification is respectfully requested.

The Examiner has rejected claims 1 and 7 under 35 U.S.C. §102(e) as allegedly being anticipated by US Patent 5,955,651 to Corrucci et al.

Claims 1 and 7-11 are rejected under 35 U.S.C. §103(a) as allegedly unpatentable over Corrucci et al. (U.S. Patent No. 5,955,651) in view of Canton F. et al. (Plant Molecular Biology, 1993, Vol. 22, pp.819-822) and Applicant's admission.

The foregoing constitutes the entirety of the objections and rejections raised in the April 11, 2003 Official Action. In light of the present amendments and the following remarks, each of the above-noted rejections under 35 U.S.C. §§ 112, first and second paragraphs, 102(e), and 103(a) is respectfully traversed.

#### **SEQUENCE LISTING**

A paper copy of the amended sequence listing in compliance with 37 C.F.R. §§1.821-1.825 is being submitted herewith providing sequence information for the nucleic acid sequence of Genbank Accession No. X69822 and the amino acid

sequence of the protein encoded thereby. Both the nucleic acid and amino acid sequences were provided when the skilled person accessed GenBank Accession number X69822 at the time the application was filed. Accordingly, Applicants submit that the provision of the nucleic acid and amino acid sequences in the attached sequence listing does not introduce new matter into the application. This statement provides the requisite evidence to support entry of the sequence into the application (see MPEP 608.01(p), which discusses the incorporation of essential material into the specification).

The sequence listing is being submitted in both paper copy and computer readable form under a separate cover in order to facilitate entry of the same into the application. Entry of the sequence listing is respectfully requested.

**CLAIMS 2, 7, 11, 12, 18, AND 21 AS AMENDED FULLY COMPLY  
WITH THE DEFINITIVENESS REQUIREMENT OF U.S.C. §112,**

**SECOND PARAGRAPH**

It is the Examiner's position that the phrase "Genbank Accession No. X69822" renders claims 2 and 7 indefinite. Applicants disagree with the Examiner's assertion. However, in order to expedite prosecution, claims 2 and 7 have been amended to replace the phrase "Genbank Accession No. X69822" with "SEQ ID NO: 3". The cancellation of the b) clause from claim 7 renders the Examiner's rejection of this claim moot. The substitute sequence listing submitted herewith designates the nucleic acid provided in Genbank Accession No. X69822, as SEQ ID NO: 3. The amino acid sequence encoded thereby is designated as SEQ ID NO: 4. It is respectfully requested that the amendments to the specification inserting these sequence identifiers where appropriate be entered in the above-identified application.

The Examiner further rejects claim 7 asserting that the phrase "encodes a protein having enzymatic function" renders

the metes and bounds of the claim unclear. Claim 7 has been amended to recite that the sequence "encodes a protein having glutamate synthetase activity", which is clear and definite.

Applicants have also followed the Examiner's helpful suggestion made the following claim amendments: 1) The "the" has been replaced with an "a" in claim 11; 2) "said plant" has been replaced with "a plant" in claim 12; and 3) claim 18 has been amended to recite "wherein the transforming is by *Agrobacterium tumefaciens* mediated transformation".

The Examiner also asserts that claim 19 is improperly dependent. Inasmuch as claim 19 was canceled in the previous response, this rejection of claim 19 is moot.

Additionally, the Examiner maintains the rejection of claim 21 asserting that the phrase "a reproductive unit" is indefinite. Applicants hereby reiterate the position that "a reproductive unit" is clear and definite to those skilled in the art of plant biology. See U.S. Patent Nos. 5,861,542 and 6,194,167. In the '542 patent, a "reproductive unit" of a plant was defined as "any totipotent part or tissue of the plant from which one can obtain a progeny of the plant, including, for example, seeds, cuttings, buds, bulbs, somatic embryos, etc." In the '167 patent, the term "a reproductive unit" of a plant was similarly defined as "any totipotent part or tissue of the plant from which one can obtain a progeny of the plant, including, for example, seeds, cuttings, tubers, buds, bulbs, somatic embryos, cultured cells (e.g., callus or suspension cultures), etc." It is a well settled premise in patent law that "a patent need not teach, and preferably omits, what is well known in the art." Lindemann

Maschinenfabrik v. American Hoist and Derrick, 221 USPQ 481, 489 (Fed. Cir. 1984). The skilled person readily appreciates that the phrase encompasses any unit from a plant from which progeny may be obtained. In light of all the foregoing, it is

clear that the metes and bounds of the phrase "reproductive unit" are clear to those skilled the relevant art.

In view of the forgoing remarks and the claim amendments, it is respectfully submitted that claims 2, 7, 11, 12, 18, and 21 as amended fully comply with the requirements set forth in 35 U.S.C. §112, second paragraph. Accordingly, withdrawal of the above-mentioned rejections is respectfully requested.

**CLAIMS 1 AND 7 AS AMENDED ARE NOT ANTICIPATED BY CORUZZI ET AL.**

The Examiner asserts that because Coruzzi et al. teach plant expression cassettes Z3 and Z17 comprising the pBIN vector with a 35S promoter operably linked to a pea glutamine synthetase (GS) cDNA having at least 70% sequence identity for both the protein and nucleic acid sequences provided in GenBank Accession number X69822, and a NOS terminator, this reference anticipates the subject matter of claims 1 and 7.

Applicants respectfully submit that claim 1 as amended is directed to plant expression cassettes comprising a GS coding sequence from gymnosperm. The GS used in the vectors of Coruzzi et al. is from pea, an angiosperm. Claim 7 has been amended to include a reference to SEQ ID NO: 3 which is isolated from gymnosperm. Inasmuch as Coruzzi et al. do not identically disclose each and every feature of the claims as amended, Applicants respectfully submit that the §102(e) rejection of claim 1 and 7 is improper and should be withdrawn.

**AMENDED CLAIMS 1 AND 7-11 ARE NOT UNPATENTABLE OVER CORUZZI ET AL. IN VIEW OF CANTON ET AL. AND APPLICANT'S ADDMISSION**

At page 7 of the Official Action, the Examiner states that "[i]t would have been *prima facie* obvious at the time of Applicant's invention to modify the expression cassette and *Agrobacterium* vector of Coruzzi to substitute the cDNA

encoding glutamine synthetase from *Pinus sylvestris* as taught by Canton for the nucleic acid from pea because the two nucleic acids are functionally equivalent in that they both encode glutamine synthetase". The Examiner further asserts that "[i]t would have been obvious to substitute one functional equivalent for another".

Applicants respectfully submit that the foregoing assertion is erroneous on its face.

It is well known in the art that GS from angiosperm and gymnosperm plants are biochemically and functionally distinct in their regulation and expression patterns. In angiosperm plants, e.g., pea, there are two major forms of GS: a cytosolic form expressed in roots and vascular tissues, such as GS1, and a plastid form expressed in photosynthetic tissues, such as GS2. In gymnosperm plants, e.g., pine, several GS1 genes have been characterized, but GS2, the plastid form observed in angiosperm plants, does not exist. Further GS1a from pine has features quite distinct from GS1 of angiosperm plants. For example, GS1a from pine is expressed in photosynthetic tissues and its expression is correlated with plastid development (Canovas et al., *Planta* 1991;185:372-378; Canton et al., *Plant Mol. Biol.* 1993;22:819-828; and Garcia-Gutierrez et al., *Plant J.* 1998;13:187-199). Neither of these features of pine GS1a is shared with other GS1 enzymes from angiosperm species, such as pea. Therefore, the GS enzymes from gymnosperm plants are not functionally equivalent to those from angiosperm plants, e.g., pea. Accordingly, claim 1 which is directed to a vector comprising a GS coding sequence from gymnosperm plants is not rendered obvious by the disclosure in Coruzzi et al., in view of Canton et al. and applicant's remarks.

Moreover, claim 7 has been amended to recite a glutamine synthetase coding sequence having the sequence of GenBank Sequence X69822, or a glutamine synthetase coding sequence

that is at least 70% identical to GenBank Sequence X69822, or a glutamine synthetase coding sequence that hybridizes to GenBank Sequence X69822 at moderate stringency. It is submitted that the pea GS coding sequence used in Coruzzi et al., GS1A (GenBank Accession No. M20663) and GS3A (GenBank Accession No. X04763) share only a 50.2% and a 61.9% similarity with GenBank Sequence X69822, respectively (See the nucleic acid sequence alignment attached hereto Exhibits A and B).

As mentioned above, the angiosperm or pea GS enzyme encoded by the vectors of Coruzzi et al. is NOT functionally equivalent to the gymnosperm or pine GS enzyme encoded by the sequences disclosed by Canton et al. It would, therefore, NOT have been obvious to substitute the pea GS coding sequence in the vectors of Coruzzi et al. with the pine GS coding sequence in Canton et al.

To establish a *prima facie* case of obviousness, three basic criteria must be met: (1) there must be some suggestion or motivation, either in the references themselves or in the knowledge generally available to one of ordinary skill in the art, to modify the reference or to combine reference teachings; (2) there must be a reasonable expectation of success; and (3) the prior art reference (or references when combined) must teach or suggest all the claimed limitations (MPEP §2143). In the instant case, because the GS coding sequences disclosed by Coruzzi et al. and by Canton et al. are NOT functionally equivalent, there would have been NO motivation for one of ordinary skill in the art to combine the two references and to replace the pea GS coding sequence in Coruzzi et al. with the pine GS coding sequence in Canton et al. Further, no success would have been expected by one of ordinary skilled to combine the disclosure of Coruzzi et al. and Canton et al. Accordingly, the Examiner has failed to establish a *prima facie* case of obviousness.

Moreover, in *in re Papesch*, 315 F.2d 381, 137 USPQ 43 (CCPA 1963) and *Ex parte Thumm*, 132 USPQ 66 (Bd. App. 1961), the court has established that the presence of a property not possessed by the prior art is evidence of nonobviousness. In the instant case, the claimed expression vectors comprise gymnosperm or pine GS coding sequences. These expression vectors possess properties not possessed by the expression vectors of Coruzzi et al., which comprise pea GS coding sequences. Specifically, as disclosed in the paragraphs begin at page 13, line 21, end at page 14, line 37 of the present application, when the instantly claimed vectors are transferred into angiosperm plants, the gymnosperm GS1 transcripts are correctly processed by the angiosperm translational machinery and the pine GS1 polypeptide is detectable both in leaf regions enriched in photosynthetic cells and in vascular elements. This unusual accumulation of the pine GS1 in photosynthetic tissues could not have been predicted from the normal accumulation of the endogenous angiosperm enzyme in vascular tissue only. Further, Coruzzi et al. have disclosed that when the expression vectors containing angiosperm GS coding sequences, GS3A or GS1A, are transferred into *Nicotiana tabacum* line SR1, only 6/13 or 5/8, respectively, of the transgenic plants demonstrate overexpression of GS activity (See column 26, lines 19-65 and column 27, lines 25-40 of Coruzzi). However, the transformation efficiency of the presently claimed vectors is unexpectedly higher, nearly 100%.

In summary, the requirements to establish a *prima facie* case of obviousness have not been met. Neither the cited references or the knowledge available to those skilled in the art teach or suggest any motivation to combine the teachings of Coruzzi et al. and Canton et al. Moreover, neither the references or the knowledge available to those skilled in the art provide any reasonable expectation of success in

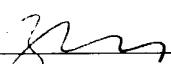
substituting the pea GS coding sequences in the vectors of Coruzzi et al. with the pine GS coding sequences in Canton et al. Finally, the vectors of the present application possess unexpected properties over those disclosed in the prior art in that the present vectors possess higher transformation efficiency and that the transgenic plants containing the same have pine GS polypeptides present in photosynthetic cells. Accordingly, Applicants respectfully submit that the rejection of claims 1 and 7-11 under 35 U.S.C. §103(a) is untenable and should be withdrawn.

#### **CONCLUSION**

In view of the amendments and remarks presented herein, it is respectfully urged that the rejections set forth in the April 11, 2003 Official Action be withdrawn and that this application be passed to issue. In the event the Examiner is not persuaded as to the allowability of any claim, and it appears that any outstanding issues may be resolved through a telephone interview, the Examiner is requested to telephone the undersigned attorney at the phone number given below.

Respectfully submitted,

DANN, DORFMAN, HERRELL AND SKILLMAN  
A Professional Corporation

By   
Tong Li  
PTO Registration No. 47,748

Telephone: (215) 563-4100

Facsimile: (215) 563-4044

Enclosures: Exhibits A and B and references describing INRA  
Clone

**EXHIBIT A**

DNA Alignment of GS1a from *P. sylvestris* (GenBank Accession No. 69822) with GS1A from *P. sativum* (GenBank Accession No. M20663)

Martinez/Needleman-Wunsch DNA Alignment

Minimum Match: 9; Gap Penalty: 1.10; Gap Length Penalty: 0.33

Seq1(1>1423) GS1a P. sylvestris	Seq2(1>1434) GS1 P. sativum M20663	Similarity Index	Gap Number	Gap Length	Consensus Length											
(1>1423)	(44>1429)	50.2	177	481	1645											
		v160	v20	v30	v40	v50	v60									
GS1a P. sylvestris	T	TTC	T	TT	CA	C A	C	CAGA	CT	TG						
				TTT												
GS1 P. sativum M20663	T	TTC	T	TT	CA	C A	C	CAGA	CT	TG						
				TTT												
		^60	^60	^70	^30	^90	^100									
		v70	v80	v90	v100	v110										
GS1a P. sylvestris	AACCTTGA	C CT	AG GA	AC A	GAGAA	TCTAT	GCAGA	TA ATATGGATTG								
GS1 P. sativum M20663	AACCTTGA	C CT	AG GA	AC A	GAGAA	TCTAT	GCAGA	TA ATATGGATTG								
		^110	^120	^130	140	150										
		v120	v130	v140	v150	v160	v170									
GS1a P. sylvestris	G GG	TC	GG	TG G	GT	AAAGC	AG A	CTCT	TC	GGAC	GT A					
GS1 P. sativum M20663	G GG	TC	GG	TG G	GT	AAAGC	AG A	CTCT	TC	GGAC	GT A					
		^160	^170	^180	^190	^200	^210									
		v170	v180	v190	v200	v210	v220									
GS1a P. sylvestris	T G C	TT	A	GAAGCT	CCCAA	TGGAA	TATGA	GG	TCAGGAC	GAACA	GCCTC					
GS1 P. sativum M20663	T G C	TT	A	GAAGCT	CCCAA	TGGAA	TATGA	GG	TCAGGAC	GAACA	GCCTC					
		^220	^230	^240	^250	^260	^270	v280								
		v230	v240	v250	v260	v270	v280									
GS1a P. sylvestris	GGACA	GA	AG	GAAGT	AT	CT	TAT	CC	ACAAAGC	AT	TTT	G GATGCAATT C				
GS1 P. sativum M20663	GGACA	GA	AG	GAAGT	AT	CT	TAT	CC	ACAAAGC	AT	TTT	G GATGCAATT C				
		^230	^240	^250	^260	^270	^280									
		v290	v300	v310	v320	v330										
GS1a P. sylvestris	AGA	GG	AA	C	CAT	T	TGGGT	AT	CGTGATGC	TAC	TCTT	TGG	GA	C	C	
GS1 P. sativum M20663	AGA	GG	AA	C	CAT	C	TGGGT	AT	CGTGATGC	TAC	TCTT	TGG	GA	C	C	
		^330	^340	^350	^360	^370	^380									
		v340	v350	v360	v370	v380	v390									
GS1a P. sylvestris	ATTCC	C	C	AA	CAA	AG	C	GCAGC	GC	AA	TTTTTA	C A	C	G	G	
GS1 P. sativum M20663	ATTCC	C	C	AA	CAA	AG	C	GCAGC	GC	AA	TTTTTA	C A	C	G	GT	
		^390	^400	^410	^420	^430	^440									
		v400	v410	v420	v430	v440										
GS1a P. sylvestris	T	GT	G	TGAAGA	ACATGTA	GG	T	T	A	A	CA	GAATA	AC	CT	GTTGCA	AAA
GS1 P. sativum M20663	T	GT	G	TGAAGA	ACATGTA	GG	T	T	A	A	CA	GAATA	AC	CT	GTTGCA	AAA
		^440	^450	^460	^470	^480	^490	v500								
		v450	v460	v470	v480	v490	v500									
GS1a P. sylvestris	G	AC	TCAA	TGGC	TCTT	GG	TGGTGG	TA	CC	GG	CCTCAGGG	CCATA				
GS1 P. sativum M20663	G	AC	TCAA	TGGC	TCTT	GG	TGGTGG	TA	CC	GG	CCTCAGGG	CCATA				
		^500	^510	^520	^530	^540	^550									
		v510	v520	v530	v540	v550	v560									
GS1a P. sylvestris	TTA	C	TGT	GG	A	G	TT	GG	G	C	TG				ACAA	
GS1 P. sativum M20663	TTA	C	TGT	GG	A	G	TT	GG	G	C	TG				ACAA	
		^560	^570	^580	^590	^600	^610									
		v560	v570	v580	v590	v600	v610									
GS1a P. sylvestris	AGCCTG	C	TT	TT	TG	GC	GG	GC	AT	CA	A	CA				

GS1 P. sativum M20663 AGCCTG C TT TT TGCC GGC AT CA A CA  
 ^610 ^620 ^620 ^630 ^640 ^650  
 v650 v660 v670 v680 v690 v700  
 GS1a P. sylvestris T CAGTCG ATCAATGGAGAAGTCATGCC GG CA TGGGAATTTCAGT GGTTC TC  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 GS1 P. sativum M20663 T CAGTCG ATCAATGGAGAAGTCATGCC GG CA TGGGAATTTCAGT GGTTC TC  
 ^640 ^650 ^660 ^670 ^680 ^690  
 v660 v670 v680 v690 v700  
 GS1a P. sylvestris AGT CGTATCTC G G GATGAG T TGG GT GCTCG T ATT TGGAGAGAT A  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 GS1 P. sativum M20663 AGT CGTATCTC G G GATGAG T TGG GT GCTCG T ATP TGGAGAGAT A  
 ^700 ^710 ^720 ^730 ^740 ^750  
 v710 v720 v730 v740 v750 v760  
 GS1a P. sylvestris C CA G GC GGTGT CCTCT T CCTTGA CCC AA CCAATT AGGG GACTGG  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 GS1 P. sativum M20663 C GA G GC GGTGT CCTCT T CCTTGA CCC AA CCAATT AGGG GACTGG  
 ^760 ^770 ^780 ^790 ^800  
 v770 v780 v790 v800 v810 v820  
 GS1a P. sylvestris AATGGTGTGG TGC CACACAAA TACAGCAGCAAGTC ATG G AAC A G G G T  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 GS1 P. sativum M20663 AATGGTGTGG TGC CACACAAA TACAGCAGCAAGTC ATG G AAG A G G G T  
 ^810 ^820 ^830 ^840 ^850 ^860  
 v830 v840 v850 v860 v870  
 GS1a P. sylvestris T GAA T AT AAGAAAGCAAT GA AA CT G AAG AGGC T G GAGCA  
 ||||| ||||| ||||| ||||| ||||| |||||  
 GS1 P. sativum M20663 T GAA T AT AAGAAAGCAAT GA AA CT G AAG AGGC T G GA3CA  
 ^870 ^880 ^890 ^900 ^910  
 v880 v890 v900 v910 v920 v930  
 GS1a P. sylvestris AT TC GC TATGG GA GG AA GAG G C G T AC GG G CACGA ACAGC  
 ||||| ||||| ||||| ||||| ||||| |||||  
 GS1 P. sativum M20663 AT TC GC TATGG GA GG AA GAG G C G T AC GG G CACGA ACAGC  
 ^920 ^930 ^940 ^950 ^960 ^970  
 v940 v950 v960 v970 v980 v990  
 GS1a P. sylvestris GACAT AATACCTT TC TGGGCTT GCAAA CGAGG CCTTC GTT G GT GG GG  
 ||||| ||||| ||||| ||||| ||||| |||||  
 GS1 P. sativum M20663 GACAT AATACCTT TC TGGGCTT GCAAA CGAGG CCTTC GTT G GT GG GG  
 ^980 ^990 ^1000 ^1010 ^1020 ^1030  
 v1000 v1010 v1020 v1030 v1040 v1050  
 GS1a P. sylvestris GACATAGA AAAGAAGG AA GGTATTGGAGGAC A  
 ||||| ||||| ||||| ||||| |||||  
 GS1 P. sativum M20663 GACATAGA AAAGAAGG AA GGTATTGGAGGAC A  
 ^1040 ^1050 ^1060 ^1070  
 v1060 v1070 v1080 v1090 v1100 v1110  
 GS1a P. sylvestris  
 GS1 P. sativum M20663  
 v1120 v1130 v1140 v1150 v1160 v1170  
 GS1a P. sylvestris  
 GS1 P. sativum M20663  
 v1180 v1190 v1200 v1210 v1220  
 GS1a P. sylvestris A C T A ATA GT TGT A T T CCA TG TT AG AG T A C T  
 ||||| ||||| ||||| ||||| |||||  
 GS1 P. sativum M20663 A C T A ATA GT TGT A T T CCA TG TT AG AG T A C T  
 ^1190 ^1190 ^1190  
 v1230 v1240 v1250 v1260 v1270  
 GS1a P. sylvestris CT T T G A ACC T AA CT TT T CT C  
 ||||| ||||| ||||| |||||  
 GS1 P. sativum M20663 CT T T G A ACC T AA CT TT T CT C  
 ^1190 ^1190 ^1190  
 v1280 v1290 v1300 v1310

GS1a P. sylvestris	TTG TAT TG A A T A A	T T TT TT T GT T	TTG T T C			
GS1 P. sativum M20663	TTG TAT TG A A T A A	T T TT TT T GT T	TTG T T C			
	^1190	^1270	^1210	^1230		
	v1320	v1330	v1340	v1350		
GS1a P. sylvestris	TTG T T T GG C A GGCTTT	G TCT TT T T	AC C TT T T TT			
GS1 P. sativum M20663	TTG T T T GG C A GGCTTT	G TCT TT T T	AC C TT T T TT			
	^1240	^1280	^1260	^1270	^1280	^1290
	v1360	v1370	v1380	v1390	v1400	
GS1a P. sylvestris	TT C C TTGT A T TAT T G CA AAT	T A A TGT				
GS1 P. sativum M20663	TT C C TTGT A T TAT T G CA AAT	T A A TGT				
	^1300	^1310	^1320	^1330	^1340	
GS1a P. sylvestris						
GS1 P. sativum M20663	^1350	^1360	^1370	^1380	^1390	^1400
	v1410	v1420				
GS1a P. sylvestris	TGAATATGA A T T T					
GS1 P. sativum M20663	TGAATATGA A T T T					
	^1410	^1420				

**EXHIBIT B**

DNA Alignment of GS1a from *P. sylvestris* (GenBank Accession No. 69822) with GS3A from *P. sativum* (GenBank Accession No. X04763)

Martinez/Needleman-Wunsch DNA Alignment

Minimum Match: 9; Gap Penalty: 1.10; Gap Length Penalty: 0.33

Seq1(1>1423) GS1a P. sylvestris	Seq2(1>1373) X04763 GS3A P. sativum	Similarity Index	Gap Number	Gap Length	Consensus Length
(193>1293) (1>1423)	(219>1206) (27>1336)	61.9 58.4	96 96	217 217	1153 1475
v79 v80 v89 v90 v100	v10 v20 v30 v40 v50 v60				
GS1a P. sylvestris T C T T C T T T CTGC G	T C T T C T T T CTGC G				
04763 GS3A P. sativum T C T T C T T T TTGC G	T C T T C T T T TTGC G				
^100 ^110 ^120	^130 ^140 ^150	^160	^170	^180	^190
v170 v180 v190 v200	v110 v120 v130 v140	v150	v160		
GS1a P. sylvestris A TA ATATGG TTGG GGATCAGG ATGA AT AG AG AAAGCCAG CTCT C GGACC GTGAGT CG T A A CTTCC AA TG GAACATA	A TA ATATGG TTGG GGATCAGG AT GA AT G AG AAAGCCAG CTCT C GGACC GTGAGT C T A A CTTCC AA TG GAACATA				
^200 ^210 ^220	^130 ^140 ^150	^160	^170	^180	^190
v270 v280 v290	v210 v220 v230	v240	v250	v260	
GS1a P. sylvestris TGA GG TC AGCAC A CA GC C AGGA A GA AG GAAGT ATT TATATCCACAAGCTAT TTC G GA CCATT C G AGAGG AA A	TGA GG TC AGCAC CA GC C AGGA A GA AG GAAGT ATT TATATCCACAAGCTAT TTC G GA CCATT C G AGAGG AA A				
04763 GS3A P. sativum A CA GC C AGGA A GA AG GAAGT ATT TATATCCACAAGCTAT TTC G GA CCATT C G AGAGG AA A	TGA GG TC AGCAC A CA GC C AGGA A GA AG GAAGT ATT TATATCCACAAGCTAT TTC G GA CCATT C G AGAGG AA A				
^300 ^310 ^320	^230 ^240 ^250	^260	^270	^280	^290
v360 v370 v380	v300 v310 v320	v330	v340	v350	
GS1a P. sylvestris A ATT TTG T AT TGTGATG TAC C CC A TGG GA C C ATT CC C CAA CAAGAG C TGC GC C AAAATTTT A AC	A ATT TTG T AT TGTGATG TAC C CC A TGG GA C C ATT CC C CAA CAAGAG C TGC GC C AAAATTTT A AC				
04763 GS3A P. sativum A ATT TTG T AT TGTGATG TAC C CC A TGG GA C C ATT CC C CAA CAAGAG C TGC GC C AAAATTTT A AC	A ATT TTG T AT TGTGATG TAC C CC A TGG GA C C ATT CC C CAA CAAGAG C TGC GC C AAAATTTT A AC				
^390 ^400 ^410	^330 ^340 ^350	^360	^370	^380	
v450 v460 v470	v390 v400 v410	v420	v430	v440	
GS1a P. sylvestris GA G TT G TG TGAAG AC ATGGTA GG TTGAACAGA TATAC CT TT CA AAAG AC TCAA TGGCC CT GG TGGCC AT	GA G TT G TG TGAAG AC ATGGTA GG TTGAACAGA TATAC CT TT CA AAAG AC TCAA TGGCC CT GG TGGCC AT				
04763 GS3A P. sativum GA G TT G TG TGAAG AC ATGGTA GG TTGAACAGA TATAC CT TT CA AAAG AC TCAA TGGCC CT GG TGGCC AT	GA G TT G TG TGAAG AC ATGGTA GG TTGAACAGA TATAC CT TT CA AAAG AC TCAA TGGCC CT GG TGGCC AT				
^480 ^490 ^500	^420 ^430 ^440	^450	^460	^470	
v550 v560 v570	v480 v490 v500	v510	v520	v530	v540

GS1a *P. sylvestris*

TGCTGG TA CC GG CAGGG CCATATTA TGTGGA TTGG GCTGA AAAGC T GGACG GACATTGTTGATGC CATTAA AG CG TG CT

04763 GS3a *P.sativum*

TGCTGG TA CC GG CAGGG CCATATTA TGTGGA TTGG GCTGA AAAGC T GGACG GACATTGTTGATGC CATTAA AG CG TG CT

560 1694 1666 1610 1620 1630 1640 1650 1660 1670

v650 v660 v670 v680 v690 v690 v610 v620 v630 v640

GS1a *P. sylvestris* T TT

C GG AT AA ATCAGTGGCATCAATGGAGA GT ATGCC GG CAGTGGAAATTCAAGT GG CC TC GT GGTATCTC GC G AGATGA G

04763 GS3a *P.sativum* T

CT C GG AT AA ATCAGTGGCATCAATGGAGA GT ATGCC GG CAGTGGAAATTCAAGT GG CC TC GT GGTATCTC GC G AGA TGAG

5670 1680 1690 1710 1610 1620 1630 1640 1650 1660

v750 v760 v770 v780 v790 v790 v710 v720 v730 v740

GS1a *P. sylvestris* T TGG G TGCTCGTT ATT T GAGAGGATTACAGA A GC GG GT T GTC T CC TTGA CGCAA GCC ATT GGG GA TGGAATGG04763 GS3a *P.sativum* T TGG G TGCTCGTT ATT T GAGAGGATTACAGA A GC GG GT T GTT T TC TTTGA CGCAA GCC ATT GGG GA TGGAATGG

5770 1780 1790 1710 1720 1730 1740 1750 1760

v780 v790 v780 v790 v780 v790 v810 v820 v830

GS1a *P. sylvestris* GCTGG GC CA CAAATT CAGGACCAA TC ATG G AA A GGAGGT CGA GTAAT AAGAA GC AT GAAAA CT G A TTGAGGCAT04763 GS3a *P.sativum* GCTGG GC CA CAAATT CAGGACCAA TC ATG G AA A GGAGGCT CGA GTAAT AAGAA GC AT GAAAA CT G A TTGAGGCAT

5870 1780 1790 1700 1710 1720 1730 1740 1750 1760

v840 v850 v860 v870 v880 v890 v900 v910 v920 v930

GS1a *P. sylvestris* AAGGA CA ATT C GC TATGG GA GGAAATGAGAGAGC CTCAC CGG A A ACA G A AC GA TA C T T TTC CT GGCGTG04763 GS3a *P.sativum* AAGGA CA ATT C GC TATGG GA GGAAATGAGAGAGC CTCAC CGG A A ACA G A AC GA TA C T T TTC CT GGCGTG

5960 1770 1780 1790 1710 1720 1730 1740 1750 1760

v1030 v1040 v1050 v1060 v1070 v1080 v1090 v1000 v1010 v1020

GS1a *P. sylvestris* T GCAAA CG GGA GTT CA TTAG GT GG G GACACAGAAAAAGA GGAAAGGTAA TTGAGGA T GA CCTGC TC AACATGGATC04763 GS3a *P.sativum* T GCAAA CG GGA GCT

CA TTAG GT GG G GACACAGAAAAAGA GGAAAGGTAA TTGAGGA T GA CCTGC TC AACATGGATC

6060 1770 1780 1790 1710 1720 1730 1740 1750 1760

v1120 v1130 v1140 v1150 v1160 v1170 v1180 v1190 v1100 v1110

GS1a *P. sylvestris* C TA T GTG ACTTC ATGATGCTGA AC ACCATTCT TGGAA AAA CA TG AG CCA AC AC C C G T CTT04763 GS3a *P.sativum* C TA T GTG ACTTC ATGATGCTGA AC ACCATTCT TGGAA AAA CA

TG AG CTA AC AC C C G T CTT

^114 ^1150 ^1150 ^1150 ^1150 ^1150  
 v1150 v1150 v1150 v1150 v1150 v1150  
 v1230 v1240 v1240 v1240 v1240 v1240  
 GS1a P. sylvestris TG  
 TTT A CCA C T AC G TA TAAT G A GT A ATGCCA T T  
 04763 GS3A P.sativum" TG TTT A CCA C T AC G TA TAAT G A GT A ATGCCA T T  
 ^1160 ^1170 ^1180 ^1190  
 v1250 v1260 v1270 v1280 v1290 v1300 v1310  
 v1320 v1330 v1340  
 GS1a P. sylvestris TATATATAT T TT T T T T T T T A T  
 04763 GS3A P.sativum" TATATATAT T TT T T T T T T T A T  
 ^1230 ^1240 ^1250 ^1260  
 v1350 v1360 v1370 v1380 v1390 v1400 v1410  
 v1420  
 GS1a P. sylvestris A T T T A T G TT A A GT T AT TATT T  
 A T T T A T G TT A A GT T AT TATT T  
 ^1270 ^1280 ^1290 ^1300 ^1310 ^1320  
 ^1330